

SEQUENCE LISTING

<110> Dale, Roderic M. K.
Arrow, Amy
Thompson, Terry

<120> Antisense Phosphodiesterase Inhibitors

<130> OLIG-003CIP

<150> 09/223,586

<151> 1998-12-30

<160> 51

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesized Oligonucleotide

<400> 1

ttagagcagg tctcgagaa gaaat

25

<210> 2

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesized Oligonucleotide

<400> 2

agcgtagca tgtatgtcac catcg

25

<210> 3

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesized Oligonucleotide

<400> 3

gcttgctgag gttctggaag atgtc

25

<210> 4

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesized Oligonucleotide

20070907 10075597 031902

<400> 4
 agagcttcct cgactcctga caat 24

 <210> 5
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthesized Oligonucleotide

 <400> 5
 atggttagagt tggttcaggct gttac 25

 <210> 6
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthesized Oligonucleotide

 <400> 6
 aggagctctt cttgatcggc cttca 25

 <210> 7
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthesized Oligonucleotide

 <400> 7
 gagaatctcc aggtccgtga aca 23

 <210> 8
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthesized Oligonucleotide

 <400> 8
 ggcgctgtag taccagtc 18

 <210> 9
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthesized Oligonucleotide

 <400> 9
 acagggacag aggtct 16

 <210> 10
 <211> 25

20070609 10:07:00

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized Oligonucleotide

<400> 10
gacttctagt cagtatcgcc aggag 25

<210> 11
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized Oligonucleotide

<400> 11
acaaatcaca gtggtgctct gcctg 25

<210> 12
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized Oligonucleotide

<400> 12
ggtcttctaa agtcatcatg taggt 25

<210> 13
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized Oligonucleotide

<400> 13
ctaaggtatc gagaatgtcc 20

<210> 14
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized Oligonucleotide

<400> 14
catgctcatc aaggatagaa tgttc 25

<210> 15
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized Oligonucleotide

2025-09-26 10:09:09

<400> 15
 gacgtttggg ttatataata cac 23

 <210> 16
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthesized Oligonucleotide

 <400> 16
 ttgttagaag ccattctcact gacag 25

 <210> 17
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthesized Oligonucleotide

 <400> 17
 atgtcaataa ccattcttcct gactg 25

 <210> 18
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthesized Oligonucleotide

 <400> 18
 tctaggagaa gaagccctga acttg 25

 <210> 19
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthesized Oligonucleotide

 <400> 19
 gacttctatg cagactctca 20

 <210> 20
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthesized Oligonucleotide

 <400> 20
 tcagtagttc gggagcattc agaag 25

 <210> 21
 <211> 18

206T220726992001

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized Oligonucleotide

<400> 21
ttctccatgc gccagaga 18

<210> 22
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized Oligonucleotide

<400> 22
cagaggagtt ccgagaca 18

<210> 23
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized Oligonucleotide

<400> 23
cgaggcttgt caccttct 18

<210> 24
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized Oligonucleotide

<400> 24
tggccctaag tcctctggtt gtcga 25

<210> 25
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized Oligonucleotide

<400> 25
gcttggtgc tcctaggc 18

<210> 26
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized Oligonucleotide

2007E597-031900

<400> 26
 atgtcctctc catgtaggtc gct 23

 <210> 27
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthesized Oligonucleotide

 <400> 27
 gttcccactt acgtccgcca 20

 <210> 28
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthesized Oligonucleotide

 <400> 28
 ccaagtctgt gaacacagcc tcgag 25

 <210> 29
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthesized Oligonucleotide

 <400> 29
 cgattgtcct ccagcgtgtc cagca 25

 <210> 30
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthesized Oligonucleotide

 <400> 30
 agtcatagct ctcttcagcc tccaa 25

 <210> 31
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthesized Oligonucleotide

 <400> 31
 ttgcactggt acgtgtcagg agaac 25

 <210> 32
 <211> 14

2025-10-20 16:59:40

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized Oligonucleotide

<400> 32
cgtgtcagga gaac 14

<210> 33
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized Oligonucleotide

<400> 33
acaggcttca gggtggcttt cctct 25

<210> 34
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized Oligonucleotide

<400> 34
gaggctttgt tgggttgctc agatc 25

<210> 35
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized Oligonucleotide

<400> 35
agataatagc acatgagtag actgg 25

<210> 36
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized Oligonucleotide

<400> 36
catctcactg acggagtgcc tggtc 25

<210> 37
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized Oligonucleotide

2025-10-10 16:59:40

<400> 37
 taatggtctt cgagagtc 18

 <210> 38
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthesized Oligonucleotide

 <400> 38
 ttgtacatca aggcaagttc agagt 25

 <210> 39
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthesized Oligonucleotide

 <400> 39
 gaagaactcc agagcttgtc acttt 25

 <210> 40
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthesized Oligonucleotide

 <400> 40
 tgatcagaaa ttgattggac acacc 25

 <210> 41
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthesized Oligonucleotide

 <400> 41
 tggtagcatt cagattgtc ctcca 25

 <210> 42
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthesized Oligonucleotide

 <400> 42
 tctcggagag atcactggag agagc 25

 <210> 43
 <211> 25

10076597.024903
 006720 46592007

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized Oligonucleotide

<400> 43
atgtgccacc gtgaaacgcc gctgt

25

<210> 44
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized Oligonucleotide

<400> 44
tcctacgtta catgtagt

18

<210> 45
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized Oligonucleotide

<400> 45
catatccagg aatgccttct

20

<210> 46
<211> 647
<212> PRT
<213> human

<400> 46
Met Pro Leu Val Asp Phe Phe Cys Glu Thr Cys Ser Lys Pro Trp Leu
1 5 10 15
Val Gly Trp Trp Asp Gln Phe Lys Arg Met Leu Asn Arg Glu Leu Thr
20 25 30
His Leu Ser Glu Met Ser Arg Ser Gly Asn Gln Val Ser Glu Tyr Ile
35 40 45
Ser Thr Thr Phe Leu Asp Lys Gln Asn Glu Val Glu Ile Pro Ser Pro
50 55 60
Thr Met Lys Glu Arg Glu Lys Gln Gln Ala Pro Arg Pro Arg Pro Ser
65 70 75 80
Gln Pro Pro Pro Pro Pro Val Pro His Leu Gln Pro Met Ser Gln Ile
85 90 95
Thr Gly Leu Lys Lys Leu Met His Ser Asn Ser Leu Asn Asn Ser Asn
100 105 110
Ile Pro Arg Phe Gly Val Lys Thr Asp Gln Glu Glu Leu Leu Ala Gln
115 120 125
Glu Leu Glu Asn Leu Asn Lys Trp Gly Leu Asn Ile Phe Cys Val Ser
130 135 140
Asp Tyr Ala Gly Gly Arg Ser Leu Thr Cys Ile Met Tyr Met Ile Phe
145 150 155 160
Gln Glu Arg Asp Leu Leu Lys Lys Phe Arg Ile Pro Val Asp Thr Met
165 170 175
Val Thr Tyr Met Leu Thr Leu Glu Asp His Tyr His Ala Asp Val Ala

[illegible]

<210> 47
 <211> 712
 <212> PRT
 <213> human

<400> 47

Met	Glu	Asn	Leu	Gly	Val	Gly	Glu	Gly	Ala	Glu	Ala	Cys	Ser	Arg	Leu	1	5	10	15
Ser	Arg	Ser	Arg	Gly	Arg	His	Ser	Met	Thr	Arg	Ala	Pro	Lys	His	Leu	20	25	30	
Trp	Arg	Gln	Pro	Arg	Arg	Pro	Ile	Arg	Ile	Gln	Gln	Arg	Phe	Tyr	Ser	35	40	45	
Asp	Pro	Asp	Lys	Ser	Ala	Gly	Cys	Arg	Glu	Arg	Asp	Leu	Ser	Pro	Arg	50	55	60	
Pro	Glu	Leu	Arg	Lys	Ser	Arg	Leu	Ser	Trp	Pro	Val	Ser	Ser	Cys	Arg	65	70	75	80
Arg	Phe	Asp	Leu	Glu	Asn	Gly	Leu	Ser	Cys	Gly	Arg	Arg	Ala	Leu	Asp	85	90	95	
Pro	Gln	Ser	Ser	Pro	Gly	Leu	Gly	Arg	Ile	Met	Gln	Ala	Pro	Val	Pro	100	105	110	
His	Ser	Gln	Arg	Arg	Glu	Ser	Phe	Leu	Tyr	Arg	Ser	Asp	Ser	Asp	Tyr	115	120	125	
Glu	Leu	Ser	Pro	Lys	Ala	Met	Ser	Arg	Asn	Ser	Ser	Val	Ala	Ser	Asp	130	135	140	
Leu	His	Gly	Glu	Asp	Met	Ile	Val	Thr	Pro	Phe	Ala	Gln	Val	Leu	Ala	145	150	155	160
Ser	Leu	Arg	Thr	Val	Arg	Ser	Asn	Val	Ala	Ala	Leu	Ala	Arg	Gln	Gln	165	170	175	
Cys	Leu	Gly	Ala	Ala	Lys	Gln	Gly	Pro	Val	Gly	Asn	Pro	Ser	Ser	Ser	180	185	190	
Asn	Gln	Leu	Pro	Pro	Ala	Glu	Asp	Thr	Gly	Gln	Lys	Leu	Ala	Leu	Glu	195	200	205	
Thr	Leu	Asp	Glu	Leu	Asp	Trp	Cys	Leu	Asp	Gln	Leu	Glu	Thr	Leu	Gln	210	215	220	
Thr	Arg	His	Ser	Val	Gly	Glu	Met	Ala	Ser	Asn	Lys	Phe	Lys	Arg	Ile	225	230	235	240
Leu	Asn	Arg	Glu	Leu	Thr	His	Leu	Ser	Glu	Thr	Ser	Arg	Ser	Gly	Asn	245	250	255	
Gln	Val	Ser	Glu	Tyr	Ile	Ser	Arg	Thr	Phe	Leu	Asp	Gln	Gln	Thr	Glu	260	265	270	
Val	Glu	Leu	Pro	Lys	Val	Thr	Ala	Glu	Glu	Ala	Pro	Gln	Pro	Met	Ser	275	280	285	
Arg	Ile	Ser	Gly	Leu	His	Gly	Leu	Cys	His	Ser	Ala	Ser	Leu	Ser	Ser	290	295	300	
Ala	Thr	Val	Pro	Arg	Phe	Gly	Val	Gln	Thr	Asp	Gln	Glu	Glu	Gln	Leu	305	310	315	320
Ala	Lys	Glu	Leu	Glu	Asp	Thr	Asn	Lys	Trp	Gly	Leu	Asp	Val	Phe	Lys	325	330	335	
Val	Ala	Asp	Val	Ser	Gly	Asn	Arg	Pro	Leu	Thr	Ala	Ile	Ile	Phe	Ser	340	345	350	
Ile	Phe	Gln	Glu	Arg	Asp	Leu	Leu	Lys	Thr	Phe	Gln	Ile	Pro	Ala	Asp	355	360	365	
Thr	Leu	Ala	Thr	Tyr	Leu	Leu	Met	Leu	Glu	Gly	His	Tyr	His	Ala	Asn	370	375	380	
Val	Ala	Tyr	His	Asn	Ser	Leu	His	Ala	Ala	Asp	Val	Ala	Gln	Ser	Thr	385	390	395	400
His	Val	Leu	Leu	Ala	Thr	Pro	Ala	Leu	Glu	Ala	Val	Phe	Thr	Asp	Leu	405	410	415	
Glu	Ile	Leu	Ala	Ala	Leu	Phe	Ala	Ser	Ala	Ile	His	Asp	Val	Asp	His	420	425	430	

20070907 01:00

006720 06592007

Pro Gly Val Ser Asn Gln Phe Leu Ile Asn Thr Asn Ser Asp Val Ala
 435 440 445
 Leu Met Tyr Asn Asp Ala Ser Val Leu Glu Asn His His Leu Ala Val
 450 455 460
 Gly Phe Lys Leu Leu Gln Ala Glu Asn Cys Asp Ile Phe Gln Asn Leu
 465 470 475 480
 Ser Ala Lys Gln Arg Leu Ser Leu Arg Arg Met Val Ile Asp Met Val
 485 490 495
 Leu Ala Thr Asp Met Ser Lys His Met Asn Leu Leu Ala Asp Leu Lys
 500 505 510
 Thr Met Val Glu Thr Lys Lys Val Thr Ser Leu Gly Val Leu Leu Leu
 515 520 525
 Asp Asn Tyr Ser Asp Arg Ile Gln Val Leu Gln Asn Leu Val His Cys
 530 535 540
 Ala Asp Leu Ser Asn Pro Thr Lys Pro Leu Pro Leu Tyr Arg Gln Trp
 545 550 555 560
 Thr Asp Arg Ile Met Ala Glu Phe Phe Gln Gln Gly Asp Arg Glu Arg
 565 570 575
 Glu Ser Gly Leu Asp Ile Ser Pro Met Cys Asp Lys His Thr Ala Ser
 580 585 590
 Val Glu Lys Ser Gln Val Gly Phe Ile Asp Tyr Ile Ala His Pro Leu
 595 600 605
 Trp Glu Thr Trp Ala Asp Leu Val His Pro Asp Ala Gln Asp Leu Leu
 610 615 620
 Asp Thr Leu Glu Asp Asn Arg Glu Trp Tyr Gln Ser Lys Ile Pro Arg
 625 630 635 640
 Ser Pro Ser Asp Leu Thr Asn Pro Glu Arg Asp Gly Pro Asp Arg Phe
 645 650 655
 Gln Phe Glu Leu Thr Leu Glu Glu Ala Glu Glu Glu Asp Glu Glu Glu
 660 665 670
 Glu Glu Glu Gly Glu Glu Thr Ala Leu Ala Lys Glu Ala Leu Glu Leu
 675 680 685
 Pro Asp Thr Glu Leu Leu Ser Pro Glu Ala Gly Pro Asp Pro Gly Asp
 690 695 700
 Leu Pro Leu Asp Asn Gln Arg Thr
 705 710

<210> 48
 <211> 564
 <212> PRT
 <213> human

<400> 48
 Met Lys Glu His Gly Gly Thr Phe Ser Ser Thr Gly Ile Ser Gly Gly
 1 5 10 15
 Ser Gly Asp Ser Ala Met Asp Ser Leu Gln Pro Leu Gln Pro Asn Tyr
 20 25 30
 Met Pro Val Cys Leu Phe Ala Glu Ser Tyr Gln Lys Leu Ala Met
 35 40 45
 Glu Thr Leu Glu Glu Leu Asp Trp Cys Leu Asp Gln Leu Glu Thr Ile
 50 55 60
 Gln Thr Tyr Arg Ser Val Ser Glu Met Ala Ser Asn Lys Phe Lys Arg
 65 70 75 80
 Met Leu Asn Arg Glu Leu Thr His Leu Ser Glu Met Ser Arg Ser Gly
 85 90 95
 Asn Gln Val Ser Glu Tyr Ile Ser Asn Thr Phe Leu Asp Lys Gln Asn
 100 105 110
 Asp Val Glu Ile Pro Ser Pro Thr Gln Lys Asp Arg Glu Lys Lys Lys
 115 120 125
 Lys Gln Gln Leu Met Thr Gln Ile Ser Gly Val Lys Lys Leu Met His

130	135	140
Ser Ser Ser Leu Asn Asn Thr Ser Ile Ser Arg Phe Gly Val Asn Thr		
145	150	155
Glu Asn Glu Asp His Leu Ala Lys Glu Leu Glu Asp Leu Asn Lys Trp		
165	170	175
Gly Leu Asn Ile Phe Asn Val Ala Gly Tyr Ser His Asn Arg Pro Leu		
180	185	190
Thr Cys Ile Met Tyr Ala Ile Phe Gln Glu Arg Asp Leu Leu Lys Thr		
195	200	205
Phe Arg Ile Ser Ser Asp Thr Phe Ile Thr Tyr Met Met Thr Leu Glu		
210	215	220
Asp His Tyr His Ser Asp Val Ala Tyr His Asn Ser Leu His Ala Ala		
225	230	235
Asp Val Ala Gln Ser Thr His Val Leu Leu Ser Thr Pro Ala Leu Asp		
245	250	255
Ala Val Phe Thr Asp Leu Glu Ile Leu Ala Ala Ile Phe Ala Ala Ala		
260	265	270
Ile His Asp Val Asp His Pro Gly Val Ser Asn Gln Phe Leu Ile Asn		
275	280	285
Thr Asn Ser Glu Leu Ala Leu Met Tyr Asn Asp Glu Ser Val Leu Glu		
290	295	300
Asn His His Leu Ala Val Gly Phe Lys Leu Leu Gln Glu Glu His Cys		
305	310	315
Asp Ile Phe Met Asn Leu Thr Lys Lys Gln Arg Gln Thr Leu Arg Lys		
325	330	335
Met Val Ile Asp Met Val Leu Ala Thr Asp Met Ser Lys His Met Ser		
340	345	350
Leu Leu Ala Asp Leu Lys Thr Met Val Glu Thr Lys Lys Val Thr Ser		
355	360	365
Ser Gly Val Leu Leu Leu Asp Asn Tyr Thr Asp Arg Ile Gln Val Leu		
370	375	380
Arg Asn Met Val His Cys Ala Asp Leu Ser Asn Pro Thr Lys Ser Leu		
385	390	395
Glu Leu Tyr Arg Gln Trp Thr Asp Arg Ile Met Glu Glu Phe Phe Gln		
405	410	415
Gln Gly Asp Lys Glu Arg Glu Arg Gly Met Glu Ile Ser Pro Met Cys		
420	425	430
Asp Lys His Thr Ala Ser Val Glu Lys Ser Gln Val Gly Phe Ile Asp		
435	440	445
Tyr Ile Val His Pro Leu Trp Glu Thr Trp Ala Asp Leu Val Gln Pro		
450	455	460
Asp Ala Gln Asp Ile Leu Asp Thr Leu Glu Asp Asn Arg Asn Trp Tyr		
465	470	475
Gln Ser Met Ile Pro Gln Ser Pro Ser Pro Pro Leu Asp Glu Gln Asn		
485	490	495
Arg Asp Cys Gln Gly Leu Met Glu Lys Phe Gln Phe Glu Leu Thr Leu		
500	505	510
Asp Glu Glu Asp Ser Glu Gly Pro Glu Lys Glu Gly Glu Gly His Ser		
515	520	525
Tyr Phe Ser Ser Thr Lys Thr Leu Cys Val Ile Asp Pro Glu Asn Arg		
530	535	540
Asp Ser Leu Gly Glu Thr Asp Ile Asp Ile Ala Thr Glu Asp Lys Ser		
545	550	555
Pro Val Asp Thr		

<210> 49
 <211> 507
 <212> PRT
 <213> human

10076597 021902

<400> 49
Met Ala Ser Asn Lys Phe Lys Arg Met Leu Asn Arg Glu Leu Thr His
1 5 10 15
Leu Ser Glu Met Ser Arg Ser Gly Asn Gln Val Ser Glu Phe Ile Ser
20 25 30
Asn Thr Phe Leu Asp Lys Gln His Glu Val Glu Ile Pro Ser Pro Thr
35 40 45
Gln Lys Glu Lys Glu Lys Lys Lys Arg Pro Met Ser Gln Ile Ser Gly
50 55 60
Val Lys Lys Leu Met His Ser Ser Ser Leu Thr Asn Ser Ser Ile Pro
65 70 75 80
Arg Phe Gly Val Lys Thr Glu Gln Glu Asp Val Leu Ala Lys Glu Leu
85 90 95
Glu Asp Val Asn Lys Trp Gly Leu His Val Phe Arg Ile Ala Glu Leu
100 105 110
Ser Gly Asn Arg Pro Leu Thr Val Ile Met His Thr Ile Phe Gln Glu
115 120 125
Arg Asp Leu Leu Lys Thr Phe Lys Ile Pro Val Asp Thr Leu Ile Thr
130 135 140
Tyr Leu Met Thr Leu Glu Asp His Tyr His Ala Asp Val Ala Tyr His
145 150 155 160
Asn Asn Ile His Ala Ala Asp Val Val Gln Ser Thr His Val Leu Leu
165 170 175
Ser Thr Pro Ala Leu Glu Ala Val Phe Thr Asp Leu Glu Ile Leu Ala
180 185 190
Ala Ile Phe Ala Ser Ala Ile His Asp Val Asp His Pro Gly Val Ser
195 200 205
Asn Gln Phe Leu Ile Asn Thr Asn Ser Glu Leu Ala Leu Met Tyr Asn
210 215 220
Asp Ser Ser Val Leu Glu Asn His His Leu Ala Val Gly Phe Lys Leu
225 230 235 240
Leu Gln Glu Glu Asn Cys Asp Ile Phe Gln Asn Leu Thr Lys Lys Gln
245 250 255
Arg Gln Ser Leu Arg Lys Met Val Ile Asp Ile Val Leu Ala Thr Asp
260 265 270
Met Ser Lys His Met Asn Leu Leu Ala Asp Leu Lys Thr Met Val Glu
275 280 285
Thr Lys Lys Val Thr Ser Ser Gly Val Leu Leu Leu Asp Asn Tyr Ser
290 295 300
Asp Arg Ile Gln Val Leu Gln Asn Met Val His Cys Ala Asp Leu Ser
305 310 315 320
Asn Pro Thr Lys Pro Leu Gln Leu Tyr Arg Gln Trp Thr Asp Arg Ile
325 330 335
Met Glu Glu Phe Phe Arg Gln Gly Asp Arg Glu Arg Glu Arg Gly Met
340 345 350
Glu Ile Ser Pro Met Cys Asp Lys His Asn Ala Ser Val Glu Lys Ser
355 360 365
Gln Val Gly Phe Ile Asp Tyr Ile Val His Pro Leu Trp Glu Thr Trp
370 375 380
Ala Asp Leu Val His Pro Asp Ala Gln Asp Ile Leu Asp Thr Leu Glu
385 390 395 400
Asp Asn Arg Glu Trp Tyr Gln Ser Thr Ile Pro Gln Ser Pro Ser Pro
405 410 415
Ala Pro Asp Asp Pro Glu Glu Gly Arg Gln Gly Gln Thr Glu Lys Phe
420 425 430
Gln Phe Glu Leu Thr Leu Glu Glu Asp Gly Glu Ser Asp Thr Glu Lys
435 440 445
Asp Ser Gly Ser Gln Val Glu Glu Asp Thr Ser Cys Ser Asp Ser Lys
450 455 460
Thr Leu Arg Thr Gln Asp Ser Glu Ser Thr Glu Ile Pro Leu Asp Glu

465 470 475 480
 Gln Val Glu Glu Glu Ala Val Gly Glu Glu Glu Ser Gln Pro Glu
 485 490 495
 Ala Cys Val Ile Asp Asp Arg Ser Pro Asp Thr
 500 505

<210> 50
 <211> 745
 <212> PRT
 <213> human

<400> 50
 Met Ala Gln Gln Thr Ser Pro Asp Thr Leu Thr Val Pro Glu Val Asp
 1 5 10 15
 Asn Pro His Cys Pro Asn Pro Trp Leu Asn Glu Asp Leu Val Lys Ser
 20 25 30
 Leu Arg Glu Asn Leu Leu Gln His Glu Lys Ser Lys Thr Ala Arg Lys
 35 40 45
 Ser Val Ser Pro Lys Leu Ser Pro Val Ile Ser Pro Arg Asn Ser Pro
 50 55 60
 Arg Leu Leu Arg Arg Met Leu Leu Ser Ser Asn Ile Pro Lys Gln Arg
 65 70 75 80
 Arg Phe Thr Val Ala His Thr Cys Phe Asp Val Asp Asn Gly Thr Ser
 85 90 95
 Ala Gly Arg Ser Pro Leu Asp Pro Met Thr Ser Pro Gly Ser Gly Leu
 100 105 110
 Ile Leu Gln Ala Asn Phe Val His Ser Gln Arg Arg Glu Ser Phe Leu
 115 120 125
 Tyr Arg Ser Asp Ser Asp Tyr Asp Leu Ser Pro Lys Ser Met Ser Arg
 130 135 140
 Asn Ser Ser Ile Ala Ser Asp Ile His Gly Asp Asp Leu Ile Val Thr
 145 150 155 160
 Pro Phe Ala Gln Val Leu Ala Ser Leu Arg Thr Val Arg Asn Asn Phe
 165 170 175
 Ala Ala Leu Thr Asn Leu Gln Asp Arg Ala Pro Ser Lys Arg Ser Pro
 180 185 190
 Met Cys Asn Gln Pro Ser Ile Asn Lys Ala Thr Ile Thr Glu Glu Ala
 195 200 205
 Tyr Gln Lys Leu Ala Ser Glu Thr Leu Glu Glu Leu Asp Trp Cys Leu
 210 215 220
 Asp Gln Leu Glu Thr Leu Gln Thr Arg His Ser Val Ser Glu Met Ala
 225 230 235 240
 Ser Asn Lys Phe Lys Arg Met Leu Asn Arg Glu Leu Thr His Leu Ser
 245 250 255
 Glu Met Ser Arg Ser Gly Asn Gln Val Ser Glu Phe Ile Ser Asn Thr
 260 265 270
 Phe Leu Asp Lys Gln His Glu Val Glu Ile Pro Ser Pro Thr Gln Lys
 275 280 285
 Glu Lys Glu Lys Lys Lys Arg Pro Met Ser Gln Ile Ser Gly Val Lys
 290 295 300
 Lys Leu Met His Ser Ser Ser Leu Thr Asn Ser Ser Ile Pro Arg Phe
 305 310 315 320
 Gly Val Lys Thr Glu Gln Glu Asp Val Leu Ala Lys Glu Leu Glu Asp
 325 330 335
 Val Asn Lys Trp Gly Leu His Val Phe Arg Ile Ala Glu Leu Ser Gly
 340 345 350
 Asn Arg Pro Leu Thr Val Ile Met His Thr Ile Phe Gln Glu Arg Asp
 355 360 365
 Leu Leu Lys Thr Phe Lys Ile Pro Val Asp Thr Leu Ile Thr Tyr Leu
 370 375 380

20061220 14:59:20

Met Thr Leu Glu Asp His Tyr His Ala Asp Val Ala Tyr His Asn Asn
 385 390 395 400
 Ile His Ala Ala Asp Val Val Gln Ser Thr His Val Leu Leu Ser Thr
 405 410 415
 Pro Ala Leu Glu Ala Val Phe Thr Asp Leu Glu Ile Leu Ala Ala Ile
 420 425 430
 Phe Ala Ser Ala Ile His Asp Val Asp His Pro Gly Val Ser Asn Gln
 435 440 445
 Phe Leu Ile Asn Thr Asn Ser Glu Leu Ala Leu Met Tyr Asn Asp Ser
 450 455 460
 Ser Val Leu Glu Asn His His Leu Ala Val Gly Phe Lys Leu Leu Gln
 465 470 475 480
 Glu Glu Asn Cys Asp Ile Phe Gln Asn Leu Thr Lys Lys Gln Arg Gln
 485 490 495
 Ser Leu Arg Lys Met Val Ile Asp Ile Val Leu Ala Thr Asp Met Ser
 500 505 510
 Lys His Met Asn Leu Leu Ala Asp Leu Lys Thr Met Val Glu Thr Lys
 515 520 525
 Lys Val Thr Ser Ser Gly Val Leu Leu Leu Asp Asn Tyr Ser Asp Arg
 530 535 540
 Ile Gln Val Leu Gln Asn Met Val His Cys Ala Asp Leu Ser Asn Pro
 545 550 555 560
 Thr Lys Pro Leu Gln Leu Tyr Arg Gln Trp Thr Asp Arg Ile Met Glu
 565 570 575
 Glu Phe Phe Arg Gln Gly Asp Arg Glu Arg Glu Arg Gly Met Glu Ile
 580 585 590
 Ser Pro Met Cys Asp Lys His Asn Ala Ser Val Glu Lys Ser Gln Val
 595 600 605
 Gly Phe Ile Asp Tyr Ile Val His Pro Leu Trp Glu Thr Trp Ala Asp
 610 615 620
 Leu Val His Pro Asp Ala Gln Asp Ile Leu Asp Thr Leu Glu Asp Asn
 625 630 635 640
 Arg Glu Trp Tyr Gln Ser Thr Ile Pro Gln Ser Pro Ser Pro Ala Pro
 645 650 655
 Asp Asp Pro Glu Glu Gly Arg Gln Gly Gln Thr Glu Lys Phe Gln Phe
 660 665 670
 Glu Leu Thr Leu Glu Glu Asp Gly Glu Ser Asp Thr Glu Lys Asp Ser
 675 680 685
 Gly Ser Gln Val Glu Glu Asp Thr Ser Cys Ser Asp Ser Lys Thr Leu
 690 695 700
 Cys Thr Gln Asp Ser Glu Ser Thr Glu Ile Pro Leu Asp Glu Gln Val
 705 710 715 720
 Glu Glu Glu Ala Val Gly Glu Glu Glu Glu Ser Gln Pro Glu Ala Cys
 725 730 735
 Val Ile Asp Asp Arg Ser Pro Asp Thr
 740 745

<210> 51
 <211> 673
 <212> PRT
 <213> human

<400> 51
 Met Met His Val Asn Asn Phe Pro Phe Arg Arg His Ser Trp Ile Cys
 1 5 10 15
 Phe Asp Val Asp Asn Gly Thr Ser Ala Gly Arg Ser Pro Leu Asp Pro
 20 25 30
 Met Thr Ser Pro Gly Ser Gly Leu Ile Leu Gln Ala Asn Phe Val His
 35 40 45
 Ser Gln Arg Arg Glu Ser Phe Leu Tyr Arg Ser Asp Ser Asp Tyr Asp

10076597 021902

50	55	60
Leu Ser Pro Lys Ser Met Ser Arg Asn Ser Ser Ile Ala Ser Asp Ile		
65	70	75
His Gly Asp Asp Leu Ile Val Thr Pro Phe Ala Gln Val Leu Ala Ser		80
	85	90
Leu Arg Thr Val Arg Asn Asn Phe Ala Ala Leu Thr Asn Leu Gln Asp		95
	100	105
Arg Ala Pro Ser Lys Arg Ser Pro Met Cys Asn Gln Pro Ser Ile Asn		110
	115	120
Lys Ala Thr Ile Thr Glu Glu Ala Tyr Gln Lys Leu Ala Ser Glu Thr		125
	130	135
Leu Glu Glu Leu Asp Trp Cys Leu Asp Gln Leu Glu Thr Leu Gln Thr		140
145	150	155
Arg His Ser Val Ser Glu Met Ala Ser Asn Lys Phe Lys Arg Met Leu		160
	165	170
Asn Arg Glu Leu Thr His Leu Ser Glu Met Ser Arg Ser Gly Asn Gln		175
	180	185
Val Ser Glu Phe Ile Ser Asn Thr Phe Leu Asp Lys Gln His Glu Val		190
	195	200
Glu Ile Pro Ser Pro Thr Gln Lys Glu Lys Glu Lys Lys Arg Pro		205
	210	215
Met Ser Gln Ile Ser Gly Val Lys Lys Leu Met His Ser Ser Ser Leu		220
225	230	235
Thr Asn Ser Ser Ile Pro Arg Phe Gly Val Lys Thr Glu Gln Glu Asp		240
	245	250
Val Leu Ala Lys Glu Leu Glu Asp Val Asn Lys Trp Gly Leu His Val		255
	260	265
Phe Arg Ile Ala Glu Leu Ser Gly Asn Arg Pro Leu Thr Val Ile Met		270
	275	280
His Thr Ile Phe Gln Glu Arg Asp Leu Leu Lys Thr Phe Lys Ile Pro		285
	290	295
Val Asp Thr Leu Ile Thr Tyr Leu Met Thr Leu Glu Asp His Tyr His		300
305	310	315
Ala Asp Val Ala Tyr His Asn Asn Ile His Ala Ala Asp Val Val Gln		320
	325	330
Ser Thr His Val Leu Leu Ser Thr Pro Ala Leu Glu Ala Val Phe Thr		335
	340	345
Asp Leu Glu Ile Leu Ala Ala Ile Phe Ala Ser Ala Ile His Asp Val		350
	355	360
Asp His Pro Gly Val Ser Asn Gln Phe Leu Ile Asn Thr Asn Ser Glu		365
	370	375
Leu Ala Leu Met Tyr Asn Asp Ser Ser Val Leu Glu Asn His His Leu		380
385	390	395
Ala Val Gly Phe Lys Leu Leu Gln Glu Glu Asn Cys Asp Ile Phe Gln		400
	405	410
Asn Leu Thr Lys Lys Gln Arg Gln Ser Leu Arg Lys Met Val Ile Asp		415
	420	425
Ile Val Leu Ala Thr Asp Met Ser Lys His Met Asn Leu Leu Ala Asp		430
	435	440
Leu Lys Thr Met Val Glu Thr Lys Lys Val Thr Ser Ser Gly Val Leu		445
	450	455
Leu Leu Asp Asn Tyr Ser Asp Arg Ile Gln Val Leu Gln Asn Met Val		460
465	470	475
His Cys Ala Asp Leu Ser Asn Pro Thr Lys Pro Leu Gln Leu Tyr Arg		480
	485	490
Gln Trp Thr Asp Arg Ile Met Glu Glu Phe Phe Arg Gln Gly Asp Arg		495
	500	505
Glu Arg Glu Arg Gly Met Glu Ile Ser Pro Met Cys Asp Lys His Asn		510
	515	520
Ala Ser Val Glu Lys Ser Gln Val Gly Phe Ile Asp Tyr Ile Val His		525

530					535					540				
Pro	Leu	Trp	Glu	Thr	Trp	Ala	Asp	Leu	Val	His	Pro	Asp	Ala	Gln
545					550					555				560
Ile	Leu	Asp	Thr	Leu	Glu	Asp	Asn	Arg	Glu	Trp	Tyr	Gln	Ser	Thr
				565					570					575
Pro	Gln	Ser	Pro	Ser	Pro	Ala	Pro	Asp	Asp	Pro	Glu	Glu	Gly	Arg
			580					585					590	Gln
Gly	Gln	Thr	Glu	Lys	Phe	Gln	Phe	Glu	Leu	Thr	Leu	Glu	Glu	Asp
		595					600					605		Gly
Glu	Ser	Asp	Thr	Glu	Lys	Asp	Ser	Gly	Ser	Gln	Val	Glu	Glu	Asp
	610					615				620				Thr
Ser	Cys	Ser	Asp	Ser	Lys	Thr	Leu	Cys	Thr	Gln	Asp	Ser	Glu	Ser
625					630					635				640
Glu	Ile	Pro	Leu	Asp	Glu	Gln	Val	Glu	Glu	Glu	Ala	Val	Gly	Glu
				645				650					655	Glu
Glu	Glu	Ser	Gln	Pro	Glu	Ala	Cys	Val	Ile	Asp	Asp	Arg	Ser	Pro
			660					665					670	Asp
Thr														

10076597-031900